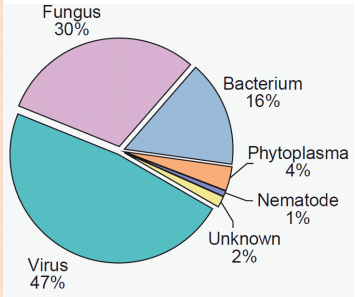
A new genus-level geminivirus lineage isolated from the South African fynbos

Pauline Bernardo[1], Emmanuel Fernandez[1], Martine Granier[1], Cica Urbino, Michel Perterschmitt[1], Darren P. Martin[2] and Philippe Roumagnac[1]

1) CIRAD/UMR BGPI, TA A-54/K, Campus international de Baillarguet, 34398 Montpellier Cedex 5, France
2)Institute of Infectious Disease and Molecular Medecine, University of Cap Town, South Africa

Viruses are the major cause of emerging diseases (47%) in plants



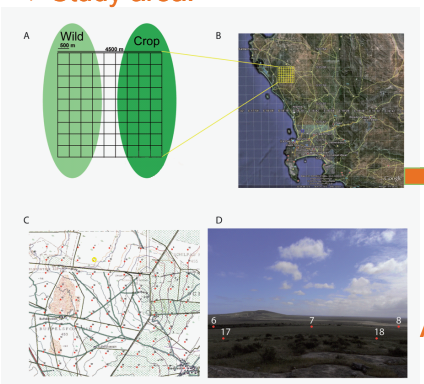
Major taxonomic groups causing emerging plants diseases (Anderson et al.,2004)

The state of the art on the diversity of plant viruses mainly concerns those causing symptoms affecting plants of economic interest. However, **wild plants have the potential to be reservoirs of viral biodiversity** which contribute to the **emergence of virus** without necessarily showing symptoms. It is very important to study the viral diversity in natural environments in order to predict future outbreaks and know how to manage them. Among the virus-DNA plants, the family ***Geminiviridae*** is known for being responsible of many plant diseases of economic interest, including tomato, cotton and cassava. Africa is a continent particularly affected by the impact of geminiviruses that threaten its main crops.

Here, we describe a new genus-level geminivirus lineage isolated from the fynbos wild ecosystem (South Africa) : *Euphorbia caput-medusae Virus* (EucmV)

Methodological approach

Study area:



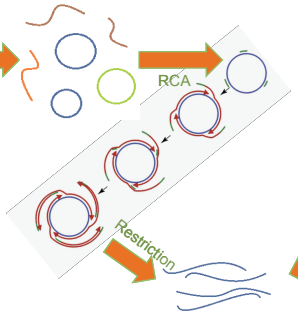
- October 2010
- 100 points
- 510 samples

Host plant: *Euphorbia caput-medusae*

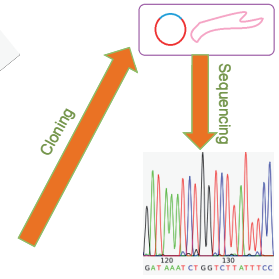
An indigenous wild species…

- Confirmation of the genera made by the sequencing of *ndhf* chloroplastic gene

Total DNA extraction, RCA, EcoR1 restriction:



Cloning and sequencing:



Operating sequence of EucmV

Genome map and ORFs:

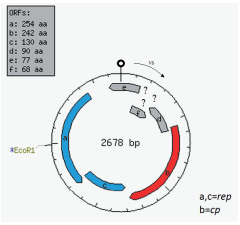
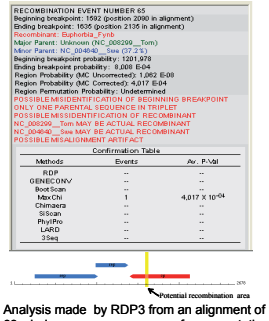


Figure made with neb cutter. The putatives ORFs were obtained with blastp on NCBI GenBank.
vs=virion sense

- Organization similar to mastrevirus:
  - -a spliced *rep* in the complementary sense (ORF a and c)
  - -a *cp* on the virion sense (ORF b)
- But a lack of *mp*
- 3 unknown ORFs

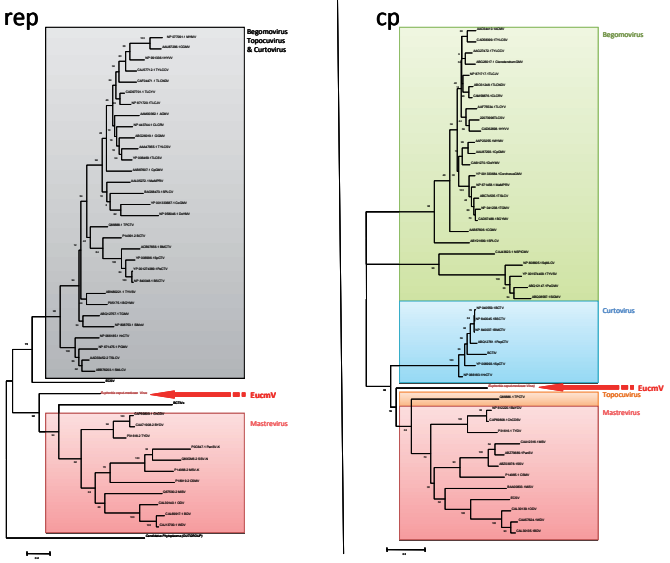
Recombinaison analysis:



Analysis made by RDP3 from an alignment of 63 whole genome sequences of representative geminivirus(CLUSTALW/ MEGA)

- Weak signal of recombination (15 aa)
- But the significance of this signal remains unclear because the sequence alignment was not optimal (because of the diversity of sequences in the *Geminiviridae* family)
- EucmV is probably not recombinant

Phylogenetic tree (Maximum likelihood):



ML trees built from an alignment on MEGA whith STATALIGN/BALIPHY with 10^6 MCMC. They represents the consensus of 1000 trees

- EucmV is probably a new genus-level of geminivirus
- He is closest to the most recent common ancestor of mastrevirus than to other geminivirus
- He is probably not recombinant, so he may give us information about ancestral characters of mastreviruses

Prospects

- Study the infectivity of EucmV
- Study the « genera concept » by finding EucmV vector and host range investigation
- Study the function of each ORF
- Confirm the phylogenetic position of EucmV within the *Geminiviridae* family

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Plant Virus Ecology Network
Workshop 4
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